APPENDIX C

PENDING CLAIMS OF SERIAL NO. 09/281,717

1. (Amended two times) A method of identifying a compound that binds to a coactivator binding site of a nuclear receptor, said method comprising:

modeling test compounds that fit spatially into the nuclear receptor coactivator binding site using an atomic structural model of the nuclear receptor coactivator binding site or portion thereof,

screening said test compounds in an assay that measures binding of a test compound to the nuclear receptor coactivator binding site, and

identifying a test compound that binds to the coactivator binding site of said nuclear receptor.

2. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454.

3. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of Vall84, Lys288, I1e302, Lys306, Leu454 and G1u457.

4. (Amended once) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of human thyroid receptor helix 3 residues I1e280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln30l, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, G1u457, Val458 and Phe459.

5. (Amended once) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues of human thyroid receptor selected from the group consisting of helix 3 residues I1e280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln301, I1e302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, Glu457, Val458 and Phe459.

6. (Amended once) The method of claim 5, wherein said amino acid residues identified by homology alignment with residues of human thyroid receptor comprise Val284, Phe293, I1e302, Leu305, and Leu454.

7. (Amended once) The method of claim 5, wherein said amino acid residues identified by homology alignment with residues of human thyroid receptor comprise Val284, Lys288, I1e302, Lys306, Leu454 and G1u457.

8. (Amended once) The method of claim 1, wherein said nuclear receptor coactivator binding site comprises amino acid residues identified by homology alignment with residues of human thyroid receptor of helix 3 residues Ile280, Thr281, Val283, Val284, Ala287, and Lys288, helix 4 residue Phe293, helix 5 residues Gln30l, Ile302, Leu305, Lys306, helix 6 residue Cys309, and helix 12 residues Pro453, Leu454, G1u457, Val458 and Phe459.

9. (Amended once) The method of any one of claims 5 through 8, wherein said nuclear receptor is selected from the group consisting of receptors for thyroid hormones, retinoids, peroxisomes, vitamin D, estrogens, glucocorticoids, progrestins, mineralcorticoids and androgens.

10. The method of claim 1, wherein said screening is in vitro.

11. The method of claim 10, wherein said screening is high throughput screening.

12. (Amended once) The method of claim 1, wherein said assay is a *in vivo* assay.

13. The method of claim 1, wherein said test compound is from a library of compounds.

14. The method of claim 1, wherein said test compound is an agonist or antagonist of coactivator binding.

15. The method of claim 14, wherein said test compound is a small organic molecule, a peptide, or peptidomimetic.

16. (Amended two times) The method of Claim 15, wherein the test compound is a peptide comprising a nuclear receptor box (NR-box) amino acid sequence or derivative thereof.

30. A compound identified according to the method of claim 1.

31. (New) The method of Claim 1 wherein the atomic coordinates of the nuclear receptor coactivator binding site are provided to a computerized modeling system.